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1

SEQUENCE LISTING

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<120> TRANSLOCATION DEPENDENT COMPLEMENTATION FOR DRUG SCREENING

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<160> 77

<170> PatentIn version 3.1

<210> 1

<211> 238

<212> PRT

<213> Aequorea victoria

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Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu
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Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys
					35			40				45			

Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe
					50				55			60			

Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln
				65			70		75				80		

His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg
				85				90				95			

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225 230 235

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Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
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Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Ser Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225 230 235

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<213> Aequorea victoria

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Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Ser His Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225 230 235

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<213> *Aequorea victoria*

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20 25 30

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35 40 45

Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 . . 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
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Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly

115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
195 200 205Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
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35 40 45Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Gly Tyr Gly Ile Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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<223>

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Ala Asn Lys Lys Glu Leu Ala Gln Leu Lys Trp Glu Leu Gln Ala Leu
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aag aag gag ctg gcc cag tag gatcc 121
Lys Lys Glu Leu Ala Gln
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<400> 8

Met Ala Gly Gly Thr Gly Ser Gly Ala Leu Lys Lys Glu Leu Gln Ala
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Asn Lys Lys Glu Leu Ala Gln Leu Lys Trp Glu Leu Gln Ala Leu Lys
20 25 30

Lys Glu Leu Ala Gln
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Met Ala Ser Glu Gln	Leu Glu Lys Lys	Leu Gln Ala	Leu Glu Lys	
1	5	10	15	

aag ctg gcc cag ctg gag tgg aag aac cag	gcc ctg gag aag aag	ctg	95
Lys Leu Ala Gln	Leu Glu Trp Lys Asn Gln	Ala Leu Glu Lys Lys	Leu
20	25	30	

gcc cag ggc ggc acc ggt tag	gatcc	121
Ala Gln Gly	Gly Thr Gly	
35		

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<212> PRT

<213> Human

<400> 10

Met Ala Ser Glu Gln	Leu Glu Lys Lys	Leu Gln Ala	Leu Glu Lys Lys	
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Leu Ala Gln	Leu Glu Trp Lys Asn Gln	Ala Leu Glu Lys Lys	Leu Ala	
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Gln Gly	Gly Thr Gly	
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Gly Ser Thr

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<211> 19

<212> PRT

<213> Human

<400> 12

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1 5 10 15

Gly Ser Thr

<210> 13

<211> 18

<212> PRT

<213> human

<400> 13

Asp Pro Ala Phe Leu Tyr Lys Val Val Ile Ser Gly Ser Gly
1 5 10 15

Ser Gly

<210> 14

<211> 18

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1 5 10 15

Ser Gly

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23

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22

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47

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<400> 19

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41

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27

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<400> 25

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<211> 44

<212> DNA

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<211> 30

<212> DNA

18

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30

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24

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21

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36

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36

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36

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34

<210> 39

<211> 57

<212> DNA

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57

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<212> DNA

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56

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catg                                              64

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gggc                                              64

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catg 64

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gggc 64

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<400> 45
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26

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<400> 48

cttccagttt tagaagctc

19

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caatataatca tcgg 74

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<400> 52
cagacaatct gtgtgggcac tcgaccgg

28

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30

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31

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25

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34

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33

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36

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34

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<211> 35

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35

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35

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29

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36

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ccttgagct ggtgtacttg gtgac

25

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Asp Pro Ala Phe Leu Tyr Lys Val Val Ile Ser Gly Ser Gly Ser Gly
1 5 10 15

Ser Gly

<210> 70

<211> 19

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<400> 70

Gly Ser Gly Ser Gly Ser Gly Asp Ile Thr Ser Leu Tyr Lys Lys Ala
1 5 10 15

Gly Ser Thr

<210> 71
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<400> 71

Asp Pro Ala Phe Leu Tyr Lys Val Val Ile Ser Gly Ser Gly
1 5 10 15

<210> 72
<211> 9
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<220>
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Gly Ser Gly Ser Gly Ser Gly Asp Leu
1 5

<210> 73
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<220>
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Asp Pro Ala Phe Leu Tyr Lys Val Val Ile Ser Gly Thr Gly Thr Gly
1 5 10 15

Thr Gly

<210> 74
<211> 19
<212> PRT
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Gly Ser Gly Ser Gly Ser Gly Asp Ile Thr Ser Leu Tyr Lys Lys Ala
1 5 10 15

Gly Ser Thr

<210> 75
<211> 12
<212> PRT
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<220>

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Asp Ile Thr Ser Leu Tyr Lys Lys Ala Gly Ser Thr
1 5 10

<210> 76
<211> 19
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<213> Artificial sequence

39

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<400> 76

Gly	Thr	Gly	Thr	Gly	Thr	Gly	Asp	Ile	Thr	Ser	Leu	Tyr	Lys	Lys	Ala
1				5					10					15	

Gly Ser Thr

<210> 77

<211> 10

<212> PRT

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<400> 77

Leu	Pro	Ser	Gly	Ser	Gly	Ser	Gly	Ser	Gly						
1				5					10						